

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hadlaczky, Gyula
Szalay, Aladar

(ii) TITLE OF THE INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES

(iii) NUMBER OF SEQUENCES: 34

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Heller Ehrman White & McAuliffe
(B) STREET: 4350 La Jolla Village Drive, 6th Floor
(C) CITY: San Diego
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92122

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/835,682
(B) FILING DATE: 10-APR-1997
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/695,191
(B) FILING DATE: 07-AUG-1996
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/682,080
(B) FILING DATE: 15-JUL-1996
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/629,822
(B) FILING DATE: 10-APR-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Seidman, Stephanie L
(B) REGISTRATION NUMBER: 33,779
(C) REFERENCE/DOCKET NUMBER: 24601-402I

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 858-450-8403
(B) TELEFAX: 858-587-5360
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1293 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:
 (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTTCATCA	TTTTTCANGT	CCTCAAGTGG	ATGTTTCTCA	TTTNCCATGA	TTTTAAGTTT	60
TCTCGCCATA	TTCCTGGTCC	TACAGTGTGC	ATTTCTCCAT	TTNCACGTT	TTNCAGTGT	120
TTCGTCATTT	TCAAGTCCTC	AAAGTGGATGT	TTCTCATTTT	CCATGAATT	CAGTTTCTCN	180
GCCATATTCC	ACGTCCTACA	GNGGACATTT	CTAAATTTC	CACCTTTTC	AGTTTCTCCTC	240
GCCATATTTC	ACGTCCTAAA	ATGTTGATTT	CTCGTTNCC	GTGATTTCA	GTTTTCTCGC	300
CAGGTCCTAC	GTCCTATAAT	GTGCAATTCT	CATTNNCAC	GTTTTTCAGT	GATTTCGTCA	360
TTTTTCAAG	TCGGCAAGTG	GATGTTCTC	ATTNNCCATG	ATTNCAGTT	TTCTTGNAAT	420
ATTCATGTC	CTACAATGAT	CATTTTAAT	TTTCCACCTT	TTCATTTTC	CACGCATAT	480
TTCATGTCCT	AAAGTGTATA	TTTCTCCTT	TCCGCGATTT	TCAGTTTCT	CGCCATATT	540
CAGGTCCTAC	AGTGTGCATT	CCTCATT	CACCTTTTC	ACTGATTTCG	TCATTTC	600
AGTCGTCAAC	TGGATCTTC	TAATTTCCA	TGATTTTCAG	TTATCTTGTC	ATATTCCATG	660
TCCTACAGTG	GACATTCTA	AATTTTCCAA	CTTTTCAAT	TTTCTCGAC	ATATTGACG	720
TGCTAAAGTG	TGTATTCTT	ATTTTCCGTG	ATTTTCAGT	TTCTCGCCAT	ATTCCAGGTC	780
CTAATAGTG	GCATTTCTA	TTTTCACGT	TTTCAGTGA	TTCGTCATT	TTTCCAGTT	840
GTCAAGGGGA	TGTTTCTCAT	TTTCCATGAG	TGTCAGTTT	TTGCTATAT	TCCATGTCCT	900
ACAGTGACAT	TTCTAAATAT	TATACCTTT	TCAGTTTTC	TCACCATATT	TCACGTCCTA	960
AAGTATATAT	TTCTCATTT	CCCTGATT	CAGTTTCCTT	GCCATATTCC	AGGTCTACA	1020
GTGTGCATT	CTCATTTC	ACGTTTTCA	GTAATTCTT	CATTTTTAA	GCCCTCAAAT	1080
GGATGTTCT	CATTTCCAT	GATTTCACT	TTTCTTGCCA	TATACCATGT	CCTACAGTGG	1140
ACATTCTAA	ATTATCCACC	TTTTCACT	TTTCATCGGC	ACATTTCACG	TCCTAAAGTG	1200
TGTATTCTA	ATTTTCAGT	ATTTTCAGT	TTCTCGCCAT	ATTCCAGGAC	CTACAGTGTG	1260
CATTCTCAT	TTTCACGTT	TTTCAGTGA	TTC			1293

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1044 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:
 (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGGCCTATGG	TGAAAAAGGA	AAATCTTCC	CCTGAAA	AGACAGAAGG	ATTCTCAGAA	60
TCTTATTG	GATGTGCGCC	CCTCAACTAA	CAGTGTGAA	GCTTTCTTT	GATAGAGCAG	120
TTTGAAACA	CTCTTTTGT	AAAATCTGCA	AGAGGATATT	TGGATAGCTT	TGAGGATTTC	180
CGTGGAAAC	GGGATTGTCT	TCATATAAAC	CCTAGACAGA	AGCATTCTCA	GAAGCTTCAT	240
TGGGATGTTT	CAGTTGAAGT	CACAGTGTG	AAACAGTCCC	TTTCATAGAG	CAGGTTGAA	300
ACACTCTTTT	TTGTAGTATC	TGGAAGTGG	CATTGGAGC	GATCTCAGGA	CTGCGGTGAA	360
AAAGGAAATA	TCTTCCAATA	AAAGCTAGAT	AGAGGCAATG	TCAGAAACCT	TTTCATGAT	420
GTATCTACTC	AGCTAACAGA	GTTGAACTT	CCTTGAGAG	AGCAGTTTG	AAACACTCTT	480
TTTGTGGAAT	CTGCAAGTGG	ATATTGTC	AGCTTGAGG	ATTCGTTGG	GAAACGGGAT	540
TACATATAAA	AAGCAGACAG	CAGCATTCCC	AGAAACTCT	TTGTGATGTT	TGCATTCAAG	600
TCACAGAGTT	GAACATTCCC	TTTCATAGAG	CAGGTTGAA	ACACACTTT	TGATGTATCT	660
GGATGTGGAC	ATTTGCAGCG	CTTTCAGGCC	TAAGGTGAA	AGGAAATATC	TTCCCTGAA	720

AACTAGACAG	AAGCATTCTC	AGAAACTTAT	TTGTGATGTG	CGCCCTCAAC	TAACAGTGT	780
GAAGCTTCT	TTTGATAGAG	GCAGTTTG	AAACACTCTT	TGTGGAATCT	GCAAGTGG	840
ATTGTCTAG	CTTTGAGGAT	TTCTTGGAA	ACGGGATTAC	ATATAAAAAG	CAGACAGCAG	900
CATTCCAGA	ATCTTGTG	TGATGTTGC	ATTCAAGTCA	CAGAGTTGAA	CATTCCCTT	960
CAGAGAGCAG	GTGGAACAC	TCTTTTATA	GTATCTGGAT	GTGGACATT	GGAGCGCTT	1020
CAGGGGGGAT	CCTCTAGAAT	TCCT				1044

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGCAGCTGG	GGGTCTCCAA	TCAGGCAGGG	GCCCCTTACT	ACTCAGATGG	GGTGGCCGAG	60
TAGGGGAAGG	GGGTGCAGGC	TGATGAGTG	GACACAGCTG	TAGGACTACC	TGGGGGCTGT	120
GGATCTATGG	GGGTGGGGAG	AAGCCCAGTG	ACAGTGCCTA	GAAGAGACAA	GGTGGCCTGA	180
GAGGGTCTGA	GGAACATAGA	GCTGGCCATG	TTGGGCCAG	GTCTCAAGCA	GGAAGTGAGG	240
AATGGGACAG	GCTTGAGGAT	ACTCTACTCA	GTAGCCAGGA	TAGCAAGGAG	GGCTTGGGT	300
TGCTATCCTG	GGGTTCAACC	CCCCAGGTG	AAGGCCCTGG	GGGAGATGGT	CCCAGGACAT	360
ATTACAATGG	ACACAGGAGG	TTGGGACACC	TGGAGTCACC	AAACAAAACC	ATGCCAAGAG	420
AGACCATGAG	TAGGGGTGTC	CAGTCCAGCC	CTCTGACTGA	GTCGATTGT	TCAAATCCAA	480
AGGGCCCTG	CTGCCACCTA	GTGGCTGATG	GCATCCACAT	GACCCCTGGC	CACACGCGTT	540
TAGGGTCTCT	GTGAAGACCA	AGATCCTTGT	TACATTGAAC	GACTCCTAAA	TGAGCAGAGA	600
TTTCCACCTA	TTCGAAACAA	TCACATAAAA	TCCATCCTGG	AAAAGCCTG	GGGGATGGCA	660
CTAAGGCTAG	GGATAGGGTG	GGATGAAGAT	TATAGTTACA	GTAAGGGGTT	TAGGTTAGG	720
GATCAACGTT	GGTTAGGAGT	TAGGGATACA	GTAGGGTACC	GTTAGGGTTA	GGGGTTAGGG	780
TTAGGGGTTA	GGGTTAGGTT	TAGGGTTAGG	GTTAGGGTTA	GGGGTTAGGG	GTTAGGGTTA	840
GGGTTAGGTT	TTGGGGTGGC	GTATTITGGT	CTTATACGCT	GTGTTCCACT	GGCAATGAAA	900
AGAGTTCTTG	TTTTCCCTTC	AGCAATTG	CATTTTAAA	AGAGTTAGC	AATTCTAACAA	960
GATATAGACC	AGCTGTGCTA	TCTCATTG	GTTTCAATT	GTAACCACAT	TGTGGTTCA	1020
ATGTGTTTAC	TTGCCATCTG	TAGATCTTCT	TTGCGTGAGG	TGTCTGTTCA	GATGTGTGTG	1080
CATTCTCTG	NTTTNGGCTG	TTAACCTTAT	TGTTTAGTT	TAATAATT	TTATATATT	1140
GAAGACAAAT	CTTTCTCAGA	TGTGTTT	CAAATATTTC	TTCATATAGA	GGCTTGCTTT	1200
TGTCTCTAAC	AAGGTCTCTT	CAGAGATAAC	TTAAATTA	GAAATCCACA	CTGTCACTTC	1260
TTTGTGTAT	ATCTACCTT	TGTGTCATT	GTTAAATTC	ATTACCAAAC	CCAAAGGCAG	1320
ATAGCTTTTC	TTCTATTGTT	TCTCTAGAA	ATTTGTATAG	TTTGCAATT	TTAGTGTAAAG	1380
GATGATTTG	AGTGATTATT	TGTGTAAGTT	GTAAAGTTT	CGTCTATATC	CATATCATT	1440
CTTATGGTTT	CCAATTAATC	GTCCTCTCAC	TATTTTGGG	AAAGACACAG	GATAGTGGGC	1500
TTTGTAGAG	TAGATAGGTA	GCTAGACATG	AACAGGAGGG	GGCCTCTGG	AAAAGGGAAA	1560
GTCGGGAAG	GCTCACCTGG	AGGACCACCA	AAAATTCA	TATTAGTAGC	ATCTCTAGTG	1620
CTGGAGTGG	TGGGCACTTG	TCAATTG	GTAGGAGGG	AAAGAGGTCC	TATGCAGAAA	1680
GAAACTCCCT	AGAACTCTC	TGAAGATG	CCAATCATTC	ACTCTGCAAT	AAAAAIGTCA	1740
GAATATTGCT	AGCTACATGC	TGATAAGGNN	AAAGGGGACA	TCTCTAAGT	AAACCTGGCA	1800
CCATAAGTAC	AGATTAGGGC	AGAGAAGGAC	ATTCAAAAGA	GGCAGGCGCA	GTAGGTACAA	1860
ACGTGATCG	TGTCAGTGTG	CCTGGGATGG	CGGGAAGGAG	GCTGGTGCA	GAGTGGATT	1920
GTATTGATCA	CCACACATAT	ACCTCAACCA	ACAGTGAGGA	GGTCCCACAA	GCCTAAGTGG	1980
GGCAAGTGG	GGAGCTAAGG	CAGTAGCAGG	AAAACAGAC	AAAGAAAACA	GGTGGAGACT	2040
TGAGACAGAG	GCAGGAATGT	GAAGAAATCC	AAAATAAAAT	TCCCTGACA	GGACTCTTAG	2100
GCTGTTAAT	GCATCGCTCA	GTCCCAC	TCCCTATT	TCTACAATAA	ACTCTTACA	2160
CTGTGTTCT	TTTCAATGAA	GTATCTG	ATCTTGTAT	TGCCTCTGG	TGAAAATGTT	2220
TCTTCCAAGT	TAAACAAGAA	CTGGGACATC	AGCTCTCCC	AGTAATAGCT	CCGTTTCAGT	2280
TTGAATTAC	AGAACTGATG	GGCTTAATAA	CTGGCGCTCT	GACTTTAGTG	GTGCAGGAGG	2340

CCGTCACACC GGGACCAAGA GTGCCCTGCC TAGTCCCCAT CTGCCCGCAG GTGGCGGCTG	2400
CCTCGACACT GACAGCAATA GGGTCCGGCA GTGTCCCCAG CTGCCAGCAG GGGGCGTACG	2460
ACGACTACAC TGTGAGCAAG AGGGCCCTGC AG	2492

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGGAATTCA TTGGGATGTT TCAGTTGA

28

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAAAGTCCC CCCTAGGAGA TCTTAAGGA

29

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGATTAAAT TAATTAAGCC CGGGC

25

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAAATTAAAT TAATTCGGGC CCGTCGA

27

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(D) OTHER INFORMATION IL-2 signal sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu

48

GTC ACA AAC AGT GCA CCT ACT
Val Thr Asn Ser Ala Pro Thr

69

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...942
- (D) OTHER INFORMATION: Renilla Reinformis Luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,418,155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGC TTA AAG ATG ACT TCG AAA GTT TAT GAT CCA GAA CAA AGG AAA CGG	48
Ser Leu Lys Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg	
1 5 10 15	
ATG ATA ACT GGT CCG CAG TGG TGG GCC AGA TGT AAA CAA ATG AAT GTT	96
Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val	
20 25 30	
CTT GAT TCA TTT ATT AAT TAT TAT GAT TCA GAA AAA CAT GCA GAA AAT	144
Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn	
35 40 45	
GCT GTT ATT TTT TTA CAT GGT AAC GAC GCG GCC TCT TCT TAT TTA TGG CGA	192
Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg	
50 55 60	
CAT GTT GTG CCA CAT ATT GAG CCA GTA GCG CGG TGT ATT ATA CCA GAT	240
His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp	
65 70 75 80	
CTT ATT GGT ATG GGC AAA TCA GGC AAA TCT GGT AAT GGT TCT TAT AGG	288
Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg	
85 90 95	
TTA CTT GAT CAT TAC AAA TAT CTT ACT GCA TGG TTG AAC TTC TTA ATT	336
Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Leu Asn Phe Leu Ile	
100 105 110	
TAC CAA AGA AGA TCA TTT TTT GTC GGC CAT GAT TGG GGT GCT TGT TTG	384
Tyr Gln Arg Arg Ser Phe Phe Val Gly His Asp Trp Gly Ala Cys Leu	
115 120 125	
GCA TTT CAT TAT AGC TAT GAG CAT CAA GAT AAG ATC AAA GCA ATA GTT	432
Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val	
130 135 140	
CAC GCT GAA AGT GTA GTA GAT GTG ATT GAA TCA TGG GAT GAA TGG CCT	480
His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro	
145 150 155 160	
GAT ATT GAA GAA GAT ATT GCG TTG ATC AAA TCT GAA GAA GGA GAA AAA	528
Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys	
165 170 175	
ATG GTT TTG GAG AAT AAC TTC TTC GTG GAA ACC ATG TTG CCA TCA AAA	576
Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys	
180 185 190	
ATC ATG AGA AAG TTA GAA CCA GAA GAA TTT GCA GCA TAT CTT GAA CCA	624

Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro			
195	200	205	
TTC AAA GAG AAA GGT GAA GTT CGT CGT CCA ACA TTA TCA TGG CCT CGT			672
Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg			
210	215	220	
GAA ATC CCG TTA GTA AAA GGT GGT AAA CCT GAC GTT GTA CAA ATT GTT			720
Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val			
225	230	235	240
AGG AAT TAT AAT GCT TAT CTA CGT GCA AGT GAT GAT TTA CCA AAA ATG			768
Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met			
245	250	255	
TTT ATT GAA TCG GAT CCA GGA TTC TTT TCC AAT GCT ATT GTT GAA GGC			816
Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly			
260	265	270	
GCC AAG AAG TTT CCT AAT ACT GAA TTT GTC AAA GTA AAA GGT CTT CAT			864
Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His			
275	280	285	
TTT TCG CAA GAA GAT GCA CCT GAT GAA ATG GGA AAA TAT ATC AAA TCG			912
Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser			
290	295	300	
TTC GTT GAG CGA GTT CTC AAA AAT GAA CAA TAA			945
Phe Val Glu Arg Val Leu Lys Asn Glu Gln			
305	310		

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTGAATTC A TGTACAGGAT GCAACTCCTG

30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGAATTCA GTAGGTGCAC TGTTTGTAC

30

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	AGAGCAGCGT	TGGGGGATAA	60
TGTCGACATT	TCCACTCCCA	ATGACGGTGA	TGTATAATGC	TCAAGTATTTC	TCCTGCTTTT	120
TTACCACTAA	CTAGGAACCTG	GGTTTGGCCT	TAATTTCAGAC	AGCCTTGGCT	CTGTCTGGAC	180
AGGTCCAGAC	GACTGACACC	ATTAACACTT	TGTCAGCCTC	AGTGAACATA	GTCATAGATG	240
AACAGGCCTC	AGCTAAATGTC	AAGATACAGA	GAGGTTCTCAT	GCTGGTTAAT	CAACTCATAG	300
ATCTTGTCCA	GATACAACTA	GATGTATTAT	GACAAATAAC	TCAGCAGGGA	TGTGAACAAA	360
AGTTTCCGGG	ATTGTGTGTT	ATTTCCATT	AGTATGTTAA	ATTTACTAGG	ACAGCTAATT	420
TGTCAAAAAG	TCTTTTCAG	TATATGTTAC	AGAATTGGAT	GGCTGAATT	GAACAGATCC	480
TTCGGGAATT	GAGACTTCAG	GTCAACTCCA	CGCGCTTGGA	CCTGTCGCTG	ACCAAAGGAT	540
TACCCAATTG	GATCTCCTCA	GCATTTTCTT	TCTTTAAAAA	ATGGGTGGGA	TTAATATTAT	600
TTGGAGATAC	ACTTTGCTGT	GGATTAGTGT	TGCTTCTTTG	ATTGGTCTGT	AAGCTTAAGG	660
CCCAAACCTAG	GAGAGACAAG	GTGGTTATTG	CCCAGGCGCT	TGCAGGACTA	GAACATGGAG	720
CTTCCCCCTGA	TATATGGTTA	TCTATGCTTA	GGCAATAGGT	CGCTGGCCAC	TCAGCTCTTA	780
TATCCCACGA	GGCTAGTCTC	ATTGTACGGG	ATAGAGTGAG	TGTGCTTCAG	CAGCCGAGA	840
GAGTTGCAAG	GCTAACGACT	GCAATGGAAA	GGCTCTGCGG	CATATATGTG	CCTATTCTAG	900
GGGGACATGT	CATCTTCAT	GAAGGTTCA	TGTCCTAGTT	CCCTTCCCCC	AGGCAAAACG	960
ACACGGGAGC	AGGTCAAGGGT	TGCTCTGGGT	AAAAGCCTGT	GAGCCTGGGA	GCTAATCCTG	1020
TACATGGCTC	CTTACCTAC	ACACTGGGG	TTGACACCTCT	ATCTCCACTC	TCATTAATAT	1080
GGGTGGCCTA	TTTGCTCTTA	TTAAAAGGAA	AGGGGGAGAT	GTTGGGAGGC	GCGCCCACAT	1140
TCGCCGTTAC	AAGATGGCGC	TGACAGCTGT	GTTCTAAAGTG	GTAAACAAAT	AATCTGCGCA	1200
TGTGCCGAGG	GTGGTTCTTC	ACTCCATGTG	CTCTGCCCTTC	CCCAGTGACGT	CAACTCGGCC	1260
GATGGGCTGC	AGCCAATCAG	GGAGTGACAC	GTCCTAGGCG	AAGGAGAATT	CTCCTTAATA	1320
GGGACGGGGT	TTCGTTCTCT	CTCTCTCTC	TGCTTCTCTC	TCTTGCTTTT	TCGCTCTCTT	1380
GCTTCCCGTA	AAGTGATAAT	GATTATCATC	TACATATCAC	AACGTGCGTG	GAGG	1434

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	AGAGCAGCGT	TGGGGGATAA	60
TGTCGACATT	TCCACTCCCA	ATGACGGTGA	TGTATAATGC	TCAAGTATTTC	TCCTGCTTTT	120
TTACCACTAA	CTAGGAACCTG	GGTTTGGCCT	TAATTTCAGAC	AGCCTTGGCT	CTGTCTGGAC	180
AGGTCCAGAT	ACAACTAGAT	GTATTATGAC	AAATAACTCA	GCAGGGATGT	GAACAAAAGT	240

TTCCGGGATT	GCGTGTATT	TCCATCCAGT	ATGTTAAATT	TACTAGGGCA	GCTAATTGTT	300
CAAAAAGTCT	TTTCCAGTAT	ATGTTACAGA	ATTGGATGGC	TGAATTGAA	CAGATCCTTC	360
GGGAATTGAG	ACTTCAGGTC	AACTCCACGC	GCTTGACCT	GTCCCTGACC	AAAGGATTAC	420
CCAATTGGAT	CTCCTCAGCA	TTTCTTTCT	TTAAAAAATG	GGTGGGATTA	ATATTATTG	480
GAGATACACT	TTGCTGTGGA	TTAGTGTGTC	TTCTTGATT	GGTCTGTAAG	CTTAAGGCC	540
AAACTAGGAG	AGACAAGGTG	GTATTGCC	AGGCGCTG	AGGACTAGAA	CATGGAGCTT	600
CCCCTGATAT	ATCTATGCTT	AGGCAATAGG	TCGCTGCCA	CTCAGCTCTT	ATATCCCAG	660
AGGCTAGTCT	CATTGCACGG	GATAGAGTGA	GTGTGCTTC	GCAGCCCGAG	AGAGTTGCAC	720
GGCTAACGAC	TGCAATGGAA	AGGCTCTGCG	GCATATATGA	GCCTATTCTA	GGGAGACATG	780
TCATCTTCTA	AGAAGGTTGA	GTGCTTCAAGT	GTCCTTCCTC	CAGGCAAAAC	GACACGGGAG	840
CAGGTAGGG	TTGCTCTGGG	TAAAAGCCTG	TGAGCTTAAG	AGCTAATCCT	GTACATGGCT	900
CCTTACCTA	CACACTGGGG	ATTGACCTC	TATCTCCACT	CTCATTAAATA	TGGGTGGCCT	960
ATTGCTCTT	ATTAAAAGGA	AAGGGGGAGA	TGTTGGGAGC	CGCGCCCACA	TTCGCCGTTA	1020
CAAGATGGCC	CTGACAGCTG	TGTTCTAAGT	GGTAAACAAA	TAATCTGCGC	ATGCCCGAG	1080
GGTGGTTCTT	CACTCCATGT	GCTCTGCCTT	CCCCGTGACG	TCAACTCGGC	CGATGGGCTG	1140
CAGTCAATCA	GGGAGTGACA	CGTCCTAGGC	GAAGGAAAAT	TCTCCTTAAT	AGGGACGGGG	1200
TTTCGTTTT	TCTCTCTCTT	GCTTCGCTCT	CTCTTGCTTC	TTGCTCTCTT	TTCCTGAAGA	1260
TGTAAGAATA	AAGCTTGCC	GCAGAAGATT	CTGGCTGTG	GTGTTCTTCC	TGGCCGGTCG	1320
TGAGAACGCG	TCTAATAACA	ATTGGTGCGG	AAACCCGGGT	GATAATGATT	ATCATCTACA	1380
TATCACAACG	TGCGTGGAGG					1400

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	ACTTTACGGG	TCCTTCACT	60
ACAACTGCCA	CGAGGCCCG	TGCTCTGGT	ATAGATCTT	GCTGAAAAGG	CACACACATG	120
ACACATTACT	CAAGGTGGG	TCATCTGAGC	TGCAGATTCA	GCTTAATATG	AATCTGCCA	180
ATTGTGTGAA	ATCATAAAATC	TTCAAAGTGA	CACTCATTGC	CAGACACAGG	TGCCCACCTT	240
TGGCATAATA	AAACAAACACA	AATTATCTAT	TATATAAAGG	GTGTTAGAAG	ATGCTTTAGA	300
ATACAAATAA	ATCATGGTAG	ATAACAGTAA	GTTGAGAGCT	TAAATTTAAT	AAAGTGTAT	360
ACCTAATAAA	AATTAAATTA	AGAAGGTGTG	AATATACTAC	AGTAGGTAAT	TTATTTCATT	420
AATTATTTT	CTTTCTTAAT	CCTTATAAT	GTTTCTGCT	ATTGTCAATT	GCACATCCAT	480
ATGTTCAATT	CTTCACTGTG	ATGAAGAAAT	GTAGTAAATA	TACTTTCCGA	ACAAGTTGTA	540
TCAAAATATG	TACACTTGAT	TCCGTGTGTT	ACTTATCATT	TTATTATTAT	ATTGATTGCA	600
TTCCCTCGTT	ACTTGATATT	ATTACAAGGT	ACATATTAT	TCTCTCAGAT	CTTCATTATA	660
CTCTAACCAT	TTTATAACAT	ACTTTATTAA	TTCATTTCTT	ATGTGTGCTG	TGAGGCACAA	720
ATGCCAGAGA	GAACTTGAGC	AGATAAGAGG	ACAAATTGCA	AGAGTCAGTT	ACCTCCTGCT	780
GTTCCTTGG	AACTCAGGAT	CAAATTCA	TTGTCAGGCT	TGGCAGCATG	CACTTTTAC	840
CAGTGCCTCC	ATCTTGCTAG	CCCTGAACAT	CAAGCTTGC	AGACAGACAG	GCTACACTAA	900
GTGAACCTGGT	CATTACACAGC	ATGCATGGTG	ATTTATTGTT	ACTTTCTATT	CCATGCCTTT	960
ACTATTTCTA	CTAGGTGCTA	GCTAGTACTG	TATTCGAGA	TAGAAGTTAC	TGAAAGAAAA	1020
TTACATTGTT	TTCTATAGAT	CCTTGATACT	CTTTCAGCAG	ATATAGAGTT	TTAACATCAGGT	1080
CCTAGACCCCT	TTCTTCACTC	TTATTAATAA	CTAAGTACAA	ATTAAGTTA	TCCAAAACAG	1140
TACGGATGTT	GATTTGTGTC	AGTTCTACTA	TGATAATAGT	CTAGCTTCAT	AAATCTGACA	1200
CACTTATTGG	GAATGTTTT	GTAAATAAA	GATTCAAGGTG	TTACTCTAGG	TCAAGAGAAAT	1260
ATAAACATC	AGTCCCAAAT	TACAAACTTC	AATAAAAGAT	TTGACTCTCC	AGTGGTGGCA	1320
ATATAAAAGTG	ATAATGATTA	TCATCTACAT	ATCACAACGT	GCCTGGAGG		1369

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22118 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCCCT	ATCCCTAATC	CAGATGGGT	GAATAACTT	GTATAGATGT	TTGTGCATTA	60
AAAACCCCTG	AGGATCTTCA	CTCTAGGTCA	CTGTCAGCA	CTGGAACCTG	AATTGTGGCC	120
CTGAGTGATA	GGTCCTGGGA	CATATGCAGT	TCTGCACAGA	CAGACAGACA	GACAGACAGA	180
CAGACAGACA	GACAGACGTT	ACAAACAAAC	ACGTTGAGCC	GTGTGCCAAC	ACACACACAA	240
ACACCACTCT	GGCCATAATT	ATTGAGGACG	TTGATTATT	ATTCTGTGTT	TGTGAGTCTG	300
TCTGTCGTC	TGTCTGTC	TCTGTCGTC	TATCAAACCA	AAAGAAACCA	AACAAATTATG	360
CCTCCTGCG	TGCGCTCG	CCTACACAGA	GAAATGATT	CTTCAATCAA	TCTAAAACGA	420
CCTCCTAAGT	TTGCCTTTT	TCTCTTCTT	TATCTTTTC	TTTTTCTTT	TCTTCCTCCT	480
TCCCTCCCTC	CTTCCTCCCT	TCCTTCCTT	CTTCTTCTT	TTCTTCTTT	CTTACTTCT	540
TTCTTCCTT	CTTACATTTA	TTCTTTCTAT	ACATAGTTT	TTAGTGAAG	CATCCCTGAC	600
TGTCTTGAAG	ACACTTGTA	GGCCTCAATC	CTGTAAGAGC	CTTCCTCTG	TTTCAAATG	660
CTGGCATGAA	TGTTGTACCT	CACTATGACC	AGCTTAGTCT	TCAAGTCTGA	GTACTGGAA	720
AGGAGTTCCA	AGAAGACTGG	TTATATTTT	CATTTATTAT	TGCATTTAA	TTAAAATTAA	780
ATTTCACCAA	AAGAATTAG	ACTGACCAAT	TCAGAGTCTG	CGGTAAAGAA	GCATAAGGAA	840
AAAGTAGGAG	AAAACGCTGA	GGCTGTCGT	GGATGGTCGA	GGCTGCTTA	GGGAGCCTCG	900
TCACCATCT	GCACCTGCAA	ACCGGGCCAC	TAGAACCCGG	TGAAGGGAGA	AACCAAAGCG	960
ACCTGGAAAC	AATAGGTAC	ATGAAGGCCA	GCCACCTCCA	TCTTGTGTC	CGGGAGTTCA	1020
GTTAGCAGAC	AAGATGGCTG	CCATGCACAT	GTGTCCTTC	AGCTTGGTGA	GGTCAAAGTA	1080
CAACCGAGTC	ACAGAACAAAG	GAAGTATACA	CAGTGAGTTC	CAGGTAGGCC	AGAGTTTACA	1140
CAGAGAAACC	ACATCTGAA	AAAAACAAAAA	AAATAAATT	AAATAATATA	ATTTAAAAT	1200
TTAAAAAATAG	CCGGGAGTGA	TGGCGCATGT	CTTTAATCCC	AGCTCTCTC	AGGCAGAGAT	1260
GGGAGGATT	CTGAGTTTGA	GGCCAGCCTG	GTCTGCAAAG	TGAGTTCCAG	GACAGTCAGG	1320
GCTATACAGA	GAAACCCCTG	CTTGAAAACT	AAACTAAATT	AAACTAAACT	AAACTAAAAA	1380
AATATAAAAT	AAAATTTA	AAGAATTTTA	AAAACTACA	AAATCAAAC	ATAAGCCCAC	1440
GAGATGGCAA	GTAACGTCAA	TCATAGCAGA	AAATATTATC	ACACACACAC	ACACAGACTC	1500
TGTCAATAAA	TCCAATGTG	CTTCATGATG	ATCAAATTTC	GATAGTCAGT	AATACTAGAA	1560
GAATCATATG	TCTGAAAATA	AAAGCCAGAA	CCTTCTGTC	TTTGTGTTTC	TTTGCCCCA	1620
AGATAGGGTT	TCTCTCAGTG	TATCCCTGGC	ATCCCTGCCT	GGAACTTCCT	TTGTAGGTT	1680
GGTAGCCTCA	AACTCAGAGA	GGTCCTCTCT	GCCTGCCTGC	CTGCCTGCCT	GCCTGCCTGC	1740
CTGCCTGCCT	GCCTGCCTCA	CTCTTCTGC	CACCCACACA	ACCGAGTCGA	ACCTAGGATC	1800
TTTATTTCTT	TCTCTTTCTC	TCTCTTTCT	TTCTTCTTCT	CTTCTTCTTCT	TTCTTCTTCTT	1860
CTTTCTTCT	TTCTTATTCA	ATTAGTTTC	AATGTAAGTG	TGTGTTGTG	CTCTATCTGC	1920
TGCCTATAGG	CCTGCTGCG	AGGAGAGGGC	AACAGAACCT	AGGAGAACCC	ACCATGCGAGC	1980
TCTGAGAAT	AAGTGAAAAA	ACAAACAAAAA	AAGGAATT	TAATCACATA	GAATGTAGAT	2040
ATATGCCGAG	GCTGTCAGAG	TGCTTTTAA	GGCTTAGTGT	AAGTAATGAA	AATTGTTGTG	2100
TGTCTTTAT	CCAAACACAG	AAGAGAGGTG	GCTCGCCCTG	CATGTCTGTT	GTCTGCATGT	2160
AGACCAGGCT	GGCCTTGAAC	ACATTAATCT	GTCTGCCTCT	GCTTCCCTAA	TGCTGCGATT	2220
AAAGGCATGT	GCCACCACTG	CCCGGACTGA	TTTCTCTTT	TTTTTTTTT	TGGAAAATAC	2280
CTTTCTTCT	TTTTCTCTCT	CTCTTCTTC	CTTCCTTCCCT	TTCTTTCTAT	TCTTTTTTTC	2340
TTTCTTTT	CTTTTTTT	TTTTTTTAA	AATTGCTCTA	AGGTAAAGG	TGTGCTCCAC	2400
AATTGCTCTA	GCTCTGCTCT	AATTCTCTT	AAAAAAAC	AAACAAAAAA	AAAACAAAAA	2460
CAGTATGTAT	GTATGTATAT	TTAGAAGAAA	TACTAATCCA	TTAAATAACT	TTTTTCCCTA	2520
AAATTCTATG	CATTCTGTT	CCACAAAGTG	AGTTCAGGA	CTTACAGAG	AAACCCCTGTG	2580
TTCAAAATTTC	TGTGTCAG	GTCACCTGG	CTTACAAAGT	GAGTCCAAG	TCCGATAGGG	2640
CTACACAGAA	AAACCATATC	TCAGAAAAAA	AAAAGTTCC	AAACACACAC	ACACACACAC	2700
ACACACACAC	ACACACACAC	ACACACACAC	ACACACACAG	CGCGCCGCGG	CGATGAGGGG	2760
AAGTCGTGCC	TAAAATAAT	ATTTTCTGG	CCAAAGTGA	AGCAAATCAC	TATGAAGAGG	2820
TACTCCTAGA	AAAAATAAT	ACAAACGGGC	TTTTAATCA	TTCCAGCACT	GTTTAATTT	2880
AACTCTGAAT	TTAGTCTTGG	AAAAGGGGGC	GGGTGTGGGT	GAGTGAAGGGC	GAGCGAGCAG	2940
ACGGGCGGGC	GGGCGGGTGA	GTGGCCGGCG	GCGGTGGCAG	CGAGCACCAG	AAAACAACAA	3000
ACCCCAAGCG	GTAGAGTGT	TTAAAAATGA	GACCTAAATG	TGTTGGAACG	GAGGTGCCG	3060
CCACCCCTCCT	CTTCCACTGC	TTAGATGCTC	CCTTCCCTT	ACTGTGCTCC	CTTCCCTAA	3120
CTGTGCCTAA	CTGTGCCTGT	TCCTCACCC	CGCTGATTG	CCAGCGACGT	ACTTTGACTT	3180

CAAGAACGAT	TTTGCTGTT	TTCACCGCTC	CCTGTCATAC	TTTCGTTTTT	GGGTGCCCGA	3240
GTCTAGCCCG	TTCGCTATGT	TCGGGCGGGG	CGATGGGGAC	CGTTTGTGCC	ACTCAGGAGA	3300
AGTGGTGGGT	GGGTACGCTG	CTCCGTCGTG	CGTGCCTGAG	TGCCCGAAC	TGAGCTCGGG	3360
AGACCCCTCCG	GAGAGACAGA	ATGAGTGA	GAATGTGGCG	GCGCGTGACG	GATCTGTATT	3420
GGTTTGTATG	GTTGATCGAG	ACCATTGTCG	GGCGACACCT	AGTGGTGACA	AGTTTCGGGA	3480
ACGCTCCAGG	CCTCTCAGGT	TGGTACACAC	GGAGAGGGAA	GTGCCTGTGG	TGAGGCGACC	3540
AGGGTGACAG	GAGGCCGGG	AAGCAGGCGG	GAGCGTCTCG	GAGATGGTGT	CGTGTGTTAAG	3600
GACGGTCTCT	AACAAGGAGG	TCGTACAGGG	AGATGCCAA	ACGAGACCGA	GTTGCTGTAC	3660
GCCCTTTGG	GAAAATGCT	AGGGTTGGTG	GCAACGTTAC	TAGTGTGACC	AGAAGGCTTA	3720
AGTCTCTAC	CCCCCCCCCT	TTTTTTTTT	TTTCTCCAG	AAGCCCTCTC	TTGTCCCCGT	3780
CACCGGGGGC	ACCGTACATC	TGAGGCCAG	AGGACCGCAT	GGGCCCGGCT	TCCAAGCCGG	3840
TGTGGCTCGG	CCAGCTGGCG	CTTCGGGTCT	TTTTTTTTT	TTTTTTTTT	TTTCCTCCA	3900
GAAGCCTTGT	CTGTCGCTGT	CACCGGGGGC	GCTGTACTTC	TGAGGCCAG	AGGACGCGAT	3960
GGGCCCGGC	TTCCAAGCCG	GTGTGGCTCG	GCCAGCTGGA	GCTTCGGGT	TTTTTTTTT	4020
TTTTTTTTT	TTTTTTCTC	CAGAAGCCTT	GTCTGTCGT	GTCACCGGGG	GCGCTGTACT	4080
TCTGAGGCCG	AGAGGACGCG	ATGGGTCGG	TTCCAAGCCG	ATGTGGCGGG	GCCAGCTGGA	4140
GCTTCGGGTT	TTTTTTTTT	CTCCAGAAGC	CCTCTCTTGT	CCCCGTCA	GGGGCGCTG	4200
TACTCTGAG	GCCGAGAGGA	CGTGTATGGGC	CCGGGTTCCA	GCGGGATGTC	GCCCAGTCAG	4260
CTGGAGCTT	GGATCTTTT	TTTTTTTTT	CCTCCAGAAG	CCCTCTTGT	TCCCCGTAC	4320
CGGGGGCACC	TTACATCTGA	GGGGCGAGAGG	ACGTGTATGGG	TCCGGCTTCC	AAGCCGATGT	4380
GGGGGGGCCA	GCTGGAGCTT	CGGGTTTTT	TTTTTTCTC	CAGAAGCCCT	CTCTTGTCCC	4440
CGTCACCGGG	GGCGCTGTAC	TTCTGAGGCC	GAGAGGACGT	GATGGGCCCG	GGTCCAGGC	4500
GGATGTCGCC	CGGTCACTG	GAGCTTTGGA	TCATTTTT	TTTCCCTCC	AGAAGCCCTC	4560
TCTTGTCCCC	GTCACCGGGG	GCACCGTACA	TCTGAGGCCG	AGAGGACACG	ATGGGCCTGT	4620
CTTCCAAGCC	GATGTGGCCC	GGCCAGCTGG	AGCTTCGGGT	CTTTTTTTT	TTTTTTCTC	4680
CAGAACCTT	GTCTGTCGCT	GTCACCCGGG	GCGCTGTACT	TCTGAGGCCG	AGAGGACGCG	4740
ATGGGCCCGG	CTTCCAAGCC	GGTGTGGCTC	GGCCAGCTGG	AGCTTCGGGT	CTTTTTTTT	4800
TTTTTTTTT	TTCTCTCAGA	AACTTGTCT	GTGCTGTCA	CCCCGGGGC	TTGTAATTCT	4860
GATGCCGAGA	GGACGCGATG	GGCCCGTCTT	CCAGGGCGAT	GTGGCCCGGT	CAGCTGGAGC	4920
TTTGGATCTT	TTTTTTTTT	TTTCCTCTCA	GAAGCCCTCT	CTTGTCCCCG	TCACCCGGGG	4980
CACCTTACAT	CTGAGGCCCTA	GAGGACACGA	TGGGCCCGGG	TTCCAGGCCG	ATGTGGCCCG	5040
GTCAGCTGGA	GCTTTGGATC	TTTTTTTTT	TTTCCTCTCA	GAAGCCCTCT	TGTCCCCGT	5100
ACCGTGGCA	CTGTACATCT	GAGGCGGAGA	GGACATTATG	GGCCCGGCTT	CCAATCCGAT	5160
GTGGCCCGGT	CAGCTGGAGC	TTGGATCTT	ATTTTTTTT	TAATTTTTC	TTCCAGAAGC	5220
CCTCTTGTCC	CTGTACCCGG	TGGCACGGTA	CATCTGAGGC	CGAGAGGACA	TTATGGGCC	5280
GGCTTCCAGG	CCGATGTGGC	CCGGTCAGGT	GGAGCTTTGG	ATCTTTTTT	TTTTTTTCT	5340
TTTTCTCTCC	AGAACGCCCTC	TCGTCTCTG	TCACCCGGGG	CCCTGTACGT	CTGAGGCCGA	5400
GGGAAAGCTA	TGGGCGCGGT	TTCTCTTCAT	TGACCTGTC	GTCTTATCAG	TTCTCCGGGT	5460
TGTCAAGGTC	GACCAAGTGT	TCCTTGAGG	TCCGGTTCTT	TTCGTTATGG	GGTCATTTTT	5520
GGGCCACCTC	CCCAGGTATG	ACTTCCAGGC	GTCGTGCTC	GCCTGTCACT	TTCCCTCC	5580
TCTCTTTAT	GCTTGTGATC	TTTCTATCT	GTTCTTATTG	GACCTGGAGA	TAGGTACTGA	5640
CACGCTGTCC	TTTCCCTATT	AAACACTAAAG	GACACTATAA	AGAGACCCCT	TCGATTTAAG	5700
GCTGTTTGC	TTGTCAGGCC	TATTCTTTT	ACTGGCTTGG	GTCTGTCGCG	GTGCTGAA	5760
CTGTCCCCGA	GCCACGCTTC	CTGCTTCCC	GGGCTGCTG	CTTGCCTGTG	CTTGCCTGTG	5820
GCAGCTGTG	ACAACCTGGC	GCTGTACTT	TGCTGCTGT	CAGACGTTT	TCCCATTTC	5880
CCCGAGGTGT	CGTTGTCACA	CTCTGCTCGG	TTGGAATGGT	GGAGCCACGT	GTGGTTGAGG	5940
GCCACCTTAT	TTCGGCTCAC	TTTTTTTTT	TTTTTTCTC	TTGGAGTC	GAACCTCCGC	6000
TCTTTCTCT	TCCCAGGCTT	TCTTCCACAT	GCCTCCCGAG	TGCATTTC	TTTGTTTTT	6060
TTCTTTTTT	TTTTTTTTT	TTGGGGAGGT	GGAGAGTCCC	GAGTACTTCA	CTCCTGTCTG	6120
TGGTGTCCAA	GTGTTCATGC	CACGTGCC	CCGAGTGCAC	TTTTTTTGT	GGCAGTCGCT	6180
CGTTGTGTT	TCTTGTCTG	TGTCTGCC	TATCAGTAAC	TGTCTGCCC	CGCGTGTAA	6240
ACATTCCAT	CTCGCTTGT	TCTCCCGATT	GCAGCGTCGTT	GCTCACTCTT	AGATCGATGT	6300
GGTGCTCCGG	AGTTCTCTTC	GGGCCAGGGC	CAAGCCGCGC	CAGGCGAGGG	ACGGACATTC	6360
ATGGCGAATG	GCGGCCGCTC	TTCTGTTCT	GCCAGCGGGC	CCTCGTCTCT	CCACCCCATC	6420
CGTCTGCCG	TGGTGTGTTG	AAGGCAGGGG	TGGGGCTCTC	CGGGCCGACG	CTGCCCGCG	6480
CGCACTTTTC	TCAGTGGTTC	GCGTGGTCTC	TGTGGATGTG	TGAGGCGCCC	GGTTGTGCC	6540
TCACGTGTTT	CACTTTGGTC	GTGCTCGCT	TGACCATGTT	CCCAGAGTCG	GTGGATGTGG	6600
CCGGTGGCGT	TGCATACCC	TCCCAGTCTG	TGTGTGCA	CGCTGTTCT	TGTAAGCGTC	6660
GAGGTGCTCC	TGGAGCGTTC	CAGGTTGTC	TCCTAGGTGC	CTGCTTCTGA	GCTGGTGGTG	6720
GCGCTCCCCA	TTCCCTGGTG	TGCCTCCGGT	GCTCCGTCTG	GCTGTGTGCC	TTCCCGTTG	6780
TGTCTGAGAA	GCCCAGTGAGA	GGGGGGTCGA	GGAGAGAAGG	AGGGGCAAGA	CCCCCTTCT	6840
TCGTCGGGTG	AGGCGCCAC	CCCAGCAGTA	GTACGCTGT	GCCTAGGGCT	GGTGTGAGC	6900
GGTCGCGGCT	GGGGTTGGAA	AGTTCTCGA	GAGACTCATT	GCTTCCCGT	GGGGAGCTTT	6960
GAGAGGCCCTG	GCTTTGGGG	GGGACCGGGT	GCAGGGTCTC	CCCTGTCCGC	GGATGCTCAG	7020
AATGCCCTTG	GAAGAGAAC	TTCTGTTGC	CGCAGACCC	CCCGCGCGGT	CGCCCGCGT	7080

TTGGTCTTCT	GGTTTCCCTG	TGTGCTCGTC	GCATGCATCC	TCTCTCGGTG	GCCGGGGCTC	7140
GTCGGGGTTT	TGGGTCCGTC	CCGCCCTCAG	TGAGAAAGTT	TCCTTCTCTA	GCTATCTTCC	7200
GGAAAGGGTG	CGGGCTCTT	ACGGTCTCGA	GGGCTCTCTC	CCGAATGGTC	CCCTGGAGGG	7260
CTCGCCCCCT	GACCGCCTCC	CGCGCGCGCA	GCGTTGCTC	TCTCGTCTAC	CGCGGCCCGC	7320
GGCCTCCCCG	CTCCGAGTTC	GGGGAGGGAT	CACGCGGGC	AGAGCCTGTC	TGTCGTCCTG	7380
CCGTTGCTGC	GGAGCATGTG	GCTCGGCTTG	TGTGGTTGGT	GGCTGGGGAG	AGGGCTCCGT	7440
GCACACCCCC	CGCGTGCCTG	ACTTTCTCC	CCTCTGAGG	CCCGCCGTC	GGACGGGGTG	7500
TGGGTAGGCG	ACGGTGGGCT	CCCGGGTCCC	CACCCGTCTT	CCCGTGCCTC	ACCCGTGCCT	7560
TCCGTCGCGT	CGCTCCCTCT	CGCTCGCGTC	CACGACTTTC	CGCGCTCCCG	CGACGGCGGC	7620
CTGGCCGCCG	CGTGGTGCCTG	GCTGTGTGCT	TCTCGGGCTG	TGTGGTTGTC	TCGCCTCGCC	7680
CCCCCCTTCC	CGCGGCAGCG	TTCCCACGGC	TGGCGAAATC	GCGGGAGTCC	TCCTTCCCCT	7740
CCTCGGGGTC	GAGAGGGTCC	GTGTCCTGGCG	TTGATTGATC	TCGCTCTCGG	GGACGGGACC	7800
GTTCTGTGGG	AGAACGGCTG	TTGGCCGCGT	CCGGCGCGAC	GTCGGACGTG	GGGACCCACT	7860
GCCGCTCGGG	GGTCTTCGTC	GGTAGGCATC	GGTGTGTCGG	CATCGGTCTC	TCTCTCGTGT	7920
CGGTGTGCC	TCCTCAGGCT	CCCGGGGGGC	CGTCGTGTTT	CGGGTCGGCT	CGGCCGCTGCA	7980
GGTGTGGTGG	GAATGCTCAG	GGGAGTGGTG	CAGTGTGATT	CCCGCCGGTT	TTGCCTCGCG	8040
TGCCCTGACC	GGTCCGACGC	CCGAGCGGTC	TCTCGTCTCC	TGTGAGGAC	CCCCTCCCGG	8100
GAGGGGCCCG	TTTCGGCCGC	CCTTCCGCTC	GTGCGCGGCC	CTCGTCTCTG	TGTGTCGTT	8160
CCCCCTCCCC	GCTCGCCGCA	CGCGGTCTTT	TTTCCTCTCT	CCCCCCCCCT	CCTCTGACTG	8220
ACCCGTGGCC	GTGCTGTGCG	ACCCCCCGCA	TGGGGCGGCG	CGGGCACGTA	CGCGTCCGGG	8280
CGGTCACCGG	GGTCTTGGGG	GGGGGCGCAG	GGGTAAGAAA	GTCGGCTCGG	GGGGCGGGAG	8340
GAGCTGTGGT	TTGGAGGGCG	TCCCAGGCCCC	GGGGCGCTGG	GGGTGTCTTG	CGCGGTCTTG	8400
GAGAGGGCTG	CGTGCAGGG	GAAAAGGTTG	CCCCCGGAGG	GAAAGGGAA	AGAGGCTAGC	8460
AGTGGTCATT	GTCCCAGCG	TGTGGTGGTC	TGTTGCCGA	GTCGCTCTG	GGGGGCTCGT	8520
CCGGCCCTGT	CGTCCGTCGG	GAAGGCGCGT	TTGGGGCCT	GCGGGAGTGC	CGAGGTGGGT	8580
ACCCCTGGCGG	TGGGATTAAC	CCCGCGCGCG	TGTCCCGGTG	TGGCGGTGGG	GGCTCCGGTC	8640
GATGTCTACC	TCCCTCTCCC	CGAGGTCTCA	GGCCTCTCC	GGCGGGGCTC	TCGGCCCTCC	8700
CCTCGTTCT	CCCTCTCGCG	GGGTTCAAGT	CGCTCGTCGA	CCTCCCCCTC	TCCGTCCTTC	8760
CATCTCTCGC	GCAATGGCGC	CGCCCGAGTT	CACGGTGGGT	TCGTCCTCCG	CCTCCGCTTC	8820
TCGCCGGGGG	CTGGCCGCTG	TCCGGTCTCT	CCTGCCCGAC	CCCCGTTGGC	GTGGTCTTCT	8880
CTCGCCGGCT	TCGCGGACTC	CTGGCTTCGC	CCGGAGGGTC	AGGGGGCTTC	CCGGTTCCCC	8940
GACGTTGCGC	CTCGCTGCTG	TGTGCTTGGG	GGGGGCCCGC	TGCGGCCCTCC	GCCCGCCCGT	9000
GAGCCCCCTG	CGCACCCGCC	GGTGTGCGGT	TCGCGCCGC	GTCAGTTGG	GCCCTGGCGT	9060
TGTGTCGCGT	CGGGAGCGTG	TCCGCTCTCG	GGCGGCTAGA	CGCGGGGTGC	GCCGGGCTCC	9120
GACGGGTGGC	CTATCCAGGG	CTCGCCCCCG	CCGACCCCG	CCTGCCCGTC	CCGGTGGTGG	9180
TCGTTGGTGT	GGGGAGGTAA	TGGTGTCTAC	GGTCATTCCC	TCGGCGTGG	TTTGACTGTC	9240
TCGCGGGTGT	CGCGCGTCTC	TTCCCGCAA	CCCCCACGCG	AACCCACAC	CCTGCTCTCC	9300
CGGCCGGTGT	CGGTGCGACGT	TCCGGCTCTC	CCGATGCCGA	GGGGTTTGGG	ATTGTGCGG	9360
GGGACGGAGG	GGAGAGCGGG	TAAGAGAGGT	GTCGGAGAGC	TGTCCCCGGG	CGACGCTCGG	9420
GTGCGTCTTG	CCGCGTGCCTG	GTGCGTGCCTG	ACGGGTTTTG	TCGGGACCCCG	ACGGGGTCGG	9480
TCCGGCCGCA	TGCACTCTCC	CGTTCCGCGC	GAGCGCCCGC	CCGGCTCAC	CCCGGTTTGT	9540
CCTCCCGCGA	GGCTCTCCGC	CGCCGCCGCC	TCCTCCTCT	CTCTCGCGT	CTCTGTCCCC	9600
CCTGGTCTG	TCCCACCCCC	GACGCTCCGC	TCGCGCTTCC	TTACCTGGTT	GATCTGCGCA	9660
GGTAGCATA	GCTTGTCTCA	AAAGATTAAGC	CATGCATGTC	TAAGTACGCA	CGGCGGGTAC	9720
AGTGAAACTG	CGAATGGCTC	ATTAATACG	TTATGGTTCC	TTGGTCTGCT	CGCTCCCTCTC	9780
CTACTGGAT	AACGTGGTA	ATTCTAGAC	TAATACATGC	CGACGGGGCG	TGACCCCCCT	9840
TCCCGGGGGG	GGATGCGTC	ATTATTCAGA	TCAAAACCAA	CCCGGTGAGC	TCCCTCCCCGG	9900
CTCCGGCCGG	GGGTGGGGCG	CCGGCGGCTT	GGTGACTCTA	GATAACCTCG	GGCCGATCGC	9960
ACGCCCCCGG	TGGCGCGAC	GACCCATTG	AACGCTCTGCC	CTATCAACTT	TCGATGGTAG	10020
TCGCCGTGCC	TACCATGGTG	ACCACGGGT	ACGGGGAATC	AGGGGTTCGAT	TCCGGAGAGG	10080
GAGCCTGAGA	AACGGCTACC	ACATCCAAGG	AAGGCAGCAG	GCGCGCAAAT	TACCCACTCC	10140
CGACCCGGGG	AGGTAGTGC	AAAAAATAAC	AATACAGGAC	TCTTCGAGG	CCCTGTAATT	10200
GAATGAGTC	CACTTTAAAT	CTTTAACGA	GGATCCATTG	GAGGGCAAGT	CTGGTGCCAG	10260
CAGCGCGGGT	AATTCCAGCT	CCAATAGCGT	ATATTAAAGT	TGCTGCAGGT	AAAAGCTCG	10320
TAGTTGGATC	TTGGGAGCGG	GGGGGGCGGT	CGCCCGAGG	CGAGTCACCG	CCCGTCCCCG	10380
CCCCCTGCT	CTCGGGCCCG	CCTCGATGCT	CTTAGCTGAG	TGTCGGCGG	GGCCCGAAGC	10440
GTTTACTTTG	AAAAAAATTAG	AGTGTTCAAA	GCAGGGCCGA	GCCGCGCTGGA	TACCGCAGCT	10500
AGGAATAATG	GAATAGGACC	GCGGTTCTAT	TTTGTGGTT	TTCGGAACCTG	AGGCCATGAT	10560
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TCGGAGGTT	GAAGACGATC	AGATACCGTC	GTAGTTCCGA	CCATAAACGA	TGCCGACTGG	10740
CGATGCGGGC	GCGTTATTCC	CATGACCCGC	CGGGCAGCTT	CGGGGAAACC	AAAGTCTTTG	10800
GGTTCCGGGG	GGAGTATGGT	TGCAAAGCTG	AAACTTAAAG	GAATTGACGG	AAGGGCACCA	10860
CCAGGAGTGG	GCCTGCGGCT	TAATTGACT	CAACACGGGA	AACCTCACCC	GGCCCGGACA	10920
CGGACAGGAT	TGACAGATTG	ATAGCTCTT	CTCGATTCCG	TGGGTGGTGG	TGCATGGCCG	10980

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CGCTTCAGCC	ACCCGAGATT	GAGCAATAAC	AGGTCTGTGA	TGCCCTTAGA	TGTCCGGGGC	11160
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CGCGTGCCTC	CCGGGTCCCG	TCGCCCCGCGT	GTGGAGCGAG	GTGTCTGGAG	TGAGGGTGAGA	11640
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TCCCCTCTCC	CTCGTCCGGC	TCTGACCTCG	CCACCCCTACC	GCGGCGGGCGG	CTGCTCGCGG	11760
GCGTCTGCC	TCTTCCCCTG	CCGGCTCTTC	CGTGTCTACG	AGGGGCGGTA	CGTCGTTACG	11820
GGTTTTGAC	CCGTCCCCGGG	GGCGTTCGGT	CGTCGGGGCG	CGCGCTTTGC	TCTCCCGGCA	11880
CCCATCCCCG	CCGCGGCTCT	GGCTTTCTA	CGTTGGCTGG	GGCGGTTGTC	GCCTGTTGGGG	11940
GGATGTGAGT	GTCGCGTGT	GGCTCGCCCG	TCCCGATGCC	ACGCTTTCT	GGCCTCGCGT	12000
GTCTCTCCCC	CTCTGTCTCC	GGGTACCTAG	CTGTGCGTT	CCGGCGCGGA	GGTTTAAGGA	12060
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CGGTCGTTCG	GGCGGCTCTC	CCTCAGACTC	CATGACCCCTC	CTCCCCCCCG	TGCCGCCGTT	12180
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CCCGACCCGC	GCGGCCGGCT	TGCCCAGTT	CCGCGGGTCG	GTCTGTTCGG	TGCCGGTCGT	12300
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CACGTGTCTC	GTTCGTTCC	TGCTGGCCGG	CCTGAGGCTA	CCCCTCGGT	CATCTGTTCT	12420
CCTCTCTCTC	CGGGGAGAGG	AGGGCGGTG	TCGTTGGGG	ACTGTGCCGT	CGTCAGCACC	12480
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CGTCGGTTGA	CGATCAATCG	CGTACCCCGC	TGCGGTGGGT	GCTGCGCGC	TGGGAGTTTG	12720
CTCGCAGGGC	CAACCCCCCA	ACCGGGGTGCG	GGCCCTCCGT	CTCCCGAAGT	TCAGACGTGT	12780
GGGCGGTTGT	CGGTGTGGCG	CGCGCGCCCG	CGTCGCGGAG	CCTGGTCTCC	CCCGCGCATC	12840
CGCGCTCGCG	GCTTCTTCCC	GCTCCGCGT	TCCCAGCCCTC	GCCCGTGAC	CCCGGTCTCG	12900
GCCCTCGCTC	GGCGCTCTCC	GGACCGCTGC	CTCACAGTC	TTTCTCGGT	CCGTGCCCCG	12960
TGGGAACCCA	CCGCGCCCCC	GTGGCGCCCG	GGGGTGGGCG	CCTCCGATC	TGCTCTGGTC	13020
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GGCGCCGCG	ACCCCTCCGC	TTGTGTGGAG	GGAGAGCGAG	GGCGAGAACG	GAGAGAGGTG	13260
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CCTCGGTGGG	CGCCTTCGCG	CCGCACGCGG	CCGCTAGGGG	CGGTGGGGC	CCGTGGCCCC	13380
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CCCTCCCGCC	GGCCTCTCGG	GAACCCCGTC	AGACGGTTCG	CGGGCTCGTC	CTCCCGTGC	13680
GCCGGGTGCC	GTCTCTTCCC	CGGCCCCCTC	CTCGCTCTC	TCTTCCCGCG	GCTGGCGCG	13740
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GAAGAGCCCA	GCGCCGAATC	CCCGCCGCGC	GTGCGGGCGT	GGGAAATGTG	CGTACGGAA	13920
GACCCACTCC	CCGGCGCCGC	TCGTGGGGGG	CCCAAGTCCT	TCTGATCGAG	GCCCAGCCCG	13980
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CCTGCTCAGT	ACGAGAGGAA	CCGCAGGTT	AGACATTGG	TGTATGTGCT	TGGCTGAGGA	18060
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ATTGAACTC	AGGACCCCTGG	CAGGTCAACT	GGAAAACGTG	TTTCTATAT	ATATAAAATAG	20640
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TGCTTTTTT	TTTCTTCTGA	GACAGTATT	CTCTGTGTA	CCTGGTGCCC	TGAAACTCAC	20760
TCTGTAGACC	AGCCTGGCCT	CAATCGAACT	CAGAAATCCT	CCTGCCTCTT	GTCTACCTCC	20820
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CCAGTCCCTC	CTGCCTCTG	GAAGATGTAG	GCATTGCA	GGGAAAAGCA	TTGTTTGAGA	21240
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(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCTGACACGC	TGTCCCTCTGG	CGACCTGTCG	TCGGAGAGGT	TGGGCCTCCG	GATGCGCGCG	60
GGGCTCTGGC	CTCACGGTGA	CCGGCTAGCC	GGCCCGCGCTC	CTGCCCTTGAG	CCGCCTGCCG	120
CGGCCCGCGG	GCCTGCTGTT	CTCTCGCGCG	TCCGAGCGTC	CCGACTCCCG	GTGCCGGCCC	180
GGGTCCGGGT	CTCTGACCCA	CCCGGGGGCG	GCGGGGAAGG	GGCGAGGGC	CACCGTGCC	240
CGTGCCTCT	CCGCTGCGGG	CGCCCGGGGC	GCCGCACAAC	CCCACCCGCT	GGCTCCGTGC	300
CGTGCCTGTC	AGGCCTCTC	GTCTCCGCGG	GGTTGTCCGC	CGCCCCCTTC	CCGGAGTGGG	360
GGGTGGCCGG	AGCCGATCGG	CTCGCTGGCC	GGCCGGCCTC	CGCTCCCAGG	GGGCTCTTCG	420
ATCGATGTGG	TGACGTCGTG	CTCTCCCGGG	CCGGGTCCGA	GCCGCGACGG	GCGAGGGGCG	480
GACGTTCTG	GCGAACGGGA	CCGTCCTTCT	CGCTCGGCC	GCGCGTCCC	CTCGCTCTGCT	540
CCTCTCCCCG	CCCGCCGGCC	GGCGTGTGGG	AAGGCGTGGG	GTGCGGACCC	CGGCCCCGACC	600
TCGCGCTCCC	GGCCCGCCGG	TCGCTTCCG	GGGTGCGGGC	CGGCGGGGTC	CTCTGACGCG	660
GCAGACAGCG	CTGCGCTGCG	CCTCCAGTGG	TTGTCGACTT	CGGGGGGGCC	CCCCCTCGCG	720
GCGGTGGGGG	TGCCGTCCCG	CCGGCCCGTC	GTGCTGCCCT	CTCGGGGGGG	GTTTGCAGCA	780
GCGTCGGCTC	CGCCTGGGCC	CTTGCGGTGC	TCCTGGAGCG	CTCCGGGTTG	TCCCTCAGGT	840
GCCCGAGGCC	GAACGGTGGT	GTGTCGTTCC	CGCCCCCGGC	GCCCCCTCCT	CCGGTCGCCG	900
CCGCGGTGTC	CGCGCGTGGG	TCCTGAGGG	GCTCGCGGT	GTGGGGTTCG	AGGCGGTTTG	960
AGTGAGACGA	GACGAGACGC	GCCCCTCCCA	CGCGGGGAAG	GGCGCCCGCC	TGCTCTCGGT	1020
GAGCGCACGT	CCCCTGCTCC	CCTCTGGCGG	GTGCGCGCGG	GCGTGTGAG	CGATCGCGGT	1080
GGGTTCGGGC	CGGTGTGACG	CGTGCGCCGG	CCGGCGCGCG	AGGGGCTGCC	GTTCTGCC	1140
CGACCGGTGTC	TGTGTGGGTT	GACTTCGGAG	GCGCTCTGCG	TCCGAAGGAG	GGAGGTGGGT	1200
GGACGGGGGG	GCCTGGTGGG	GTGCGCGCA	CGCGCGCACC	GGCGGGGGCC	CCGCCCTGAA	1260
CGCGAACGCT	CGAGGTGGCC	CGCGCGCAGGT	GTTTCTCTCG	ACCGCAGGGC	CCCCCTCCCT	1320
CCCCAGGGCT	CCCTCGGCCG	CTCTGCGGGC	CCGAGGAGGA	GCGGCTGGCG	GTTGGGGGGG	1380
GTGTGACCCA	CCCTCGGTGA	GAAAAGCCTT	CTCTAGCGAT	CTGAGAGGGC	TGCCTTGGGG	1440
GTACCGGATC	CCCCGGGCCG	CCGCCTCTGT	CTCTGCCCTCC	TTTATGGTAG	CGCTGCCGTA	1500
GCGACCCGCT	CGCAGAGGAC	CCTCCTCCGC	TTCCCCCTCG	ACGGGGTTGG	GGGGGAGAAG	1560
CGAGGGTTCC	GCCGGCCACC	GGGGTGGTGG	CCGAGTGCAGG	CTCGTCGCT	ACTGTGGCCC	1620
GCCGCTCCCC	CTTCCCAGTC	GGGGGAGGAT	CCCGCGCGGC	GGGGCCCGGC	GCTCCCACCC	1680
AGCGGGTTGG	GACCGCGCCG	CGGGGGGGCG	GTGGGGTGTGC	CGGCGGGGGC	CTCTGTCGGG	1740
CGCGTACCC	CTTCCTCGCC	CGAGTCGGCT	TCGGCGCCGC	TCCCGTGC	AGTCGTGACC	1800
GGTGCGACG	ACCGCGTTTG	CGTGGCACGG	GGTCGGGCC	GCCTGGCCCT	GGAAAGCGT	1860
CCACCGGTGG	GGGCGCGCCG	GTCTCCCGGA	GCGGGACCGG	GTCGGAGGAT	GGACGAGAAT	1920
CAAGAGCGAC	GGTGGTGGTG	GGCTGTGCCG	TTCGTGGCTG	CGGTCGCTCC	GGGGCCCCCG	1980
GTGGCGGGGC	CCCGGGGCTC	GCGAGGCGGT	TCTCGGTGGG	GGCCGAGGGC	CGTCGGCGT	2040
CCCAGGGCGG	GCGCCCGCGG	ACCGCCCTCG	TGTCTGTGGC	GTTGGGATCC	CGCGGCCGTG	2100
TTTCCTGGT	GGCCCCGGCG	TGCCTGAGGT	TTCTCCCCGA	GCGCGCGCCT	CTGCGGGCTC	2160
CCGGGTGCC	TTGCCCTCGC	GGTCCCCCGC	CCTCGCCCGT	CTGTGCCCTC	TTCCCCGCC	2220
GCCGCGCGCC	GATCCTCTTC	TTCCCCCGCA	GGCGCTCACC	GGCTTCACGT	CCGTTGGTGG	2280
CCCCGCGCTG	GACCGAACCC	GCGACCGCCT	CGTGGGGCGC	CGCCGCGCGC	CACTGATCGG	2340
CCCGCGGTCC	GCCTCCCCCG	GCGCGCGCCT	TGGGGACCGG	GTGCGGTGGCG	CGCCGCGTGG	2400
GGCCCGGGTGG	GCTTCCCGGA	GGGTTCCGGG	GGTCGGCCCTG	CGGCGCGTGC	GGGGGAGGAG	2460
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TCGCCGAGGG	CCGGTCGGCC	GCCCCGGGTG	CCCCCGGGTG	CGCGCGCGG	CGGTGAGGCC	2580
CCGCGCGTGT	GTCCCCGCTG	CGGTTCGGCCG	CGCTCGAGGG	GTCCCCGTGG	CGTCCTCTTC	2640
CCCGCCGGCC	GCCTTCTCTCG	CGCCTTCCCC	GTCGCCCGGG	CCTCGCCCGT	GGTCTCTCGT	2700
CTTCTCCCGG	CCCGCTCTTC	CGAACCGGGT	CGGCGCGTCC	CCCGGGTGC	CCTCGCTTCC	2760
CGGGCGCTGC	CGGGCGCTTC	CCCGAGGGCGT	CGTCGGCCGG	GGGGAGAGCC	2820	
CGTCCCTCCC	CGCTGGCGTC	GGCCCGTTCG	CGCGCGCGGT	GGCCCGCGAGC	GGGGCCCGGT	2880
GGTCCCTCCC	GGACAGCGCT	TGTCGCGACG	TGTGGCGTGG	GTGACCTCC	GCCTTGCCGG	2940
TCGCTCGCCC	TCTCCCGGGG	TCGGGGGGTG	GGGCCCCGGG	GGGGGGCTCG	GCCCCGGTCG	3000
CTGCGCTCCCG	TCCCAGGGCG	GGCGGGGGCG	GCGGGCGGCC	CTCGGTCGCC	CTCCCTTGGC	3060
CGTCGTGTGG	CGTGTGCCAC	CCCTGCGCCG	GCGCCCGCCG	GCGGGGCTCG	GAGCCGGGCT	3120
TCGGCCGGGC	CCCGGGCCCT	CGACCGGACC	GGCTGCGCGG	GCGCTGCGGC	CGCACGGCGC	3180
GACTGTCCCC	GGGCGGGGCA	CCGCGGTCCG	CCTCTCGCTC	GCGCGCCGGA	CGTCGGGGCC	3240
GCCCCCGCGG	GGGGGCGGAG	CGCCGTCCCC	GCCTCGCCGC	GGCCCGCGGG	CGCCGGCCGC	3300
GCGCGCGCGC	GCGTGGCCGC	CGGTCCCTCC	CGGCGGGCGG	GGCGGGGTGCG	GGCCGTCCGC	3360
CTCCTCGCGG	GGGGCGCGGA	CGAAGAAGCG	TCGCGGGTCT	GTGGCGCGGG	GCCCCCGGGT	3420

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CCCGTCCGTC	CGTCCGTCG	TCGTCTCCCT	CGCTTGCAGGG	CGGCCGGGCC	CGTCCTCGCG	3600
AGGCCCCCG	GCCGGCGTC	CGGCCCGTC	GGGGGCTCGC	CGCGCTCTAC	CTTACCTACC	3660
TGGTTGATCC	TGCCAGTAGC	ATATGCTTGT	CTCAAAGATT	AAGCCATGCA	TGTCTAAGTA	3720
CGCACGGCCG	GTACAGTGAA	ACTGCGAATG	GCTCATTAAA	TCAGTTATGG	TTCTTGGT	3780
CGCTCGCTCC	TCTCCTACTT	GGATAACTGT	GGTAATTCTA	GAGCTAATAC	ATGCCGACGG	3840
GCGCTGACCC	CCTTCGCGGG	GGGGATGCGC	GCATTATCA	GATCAAACACC	AACCCGGTCA	3900
GCCCTCTCC	GGCCCCGGCC	GGGGGGCGGG	CGCCGGCGGC	TTTGGTGA	CTAGATAACC	3960
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CTTTCGATGG	TAGTCGCGT	GCTTACCATG	GTGACCCACGG	GTGACGGGGA	ATCAGGGTTC	4080
GATTCCGGAG	AGGGAGCGT	AGAAACGGCT	ACCACATCCA	AGGAAGGCAG	CAGGCGCGCA	4140
AATTACCCAC	TCCCGACCCG	GGGAGGTAGT	GACGAAAAT	AACAATACAG	GACTTTTCG	4200
AGGCCCTGTA	ATTGGAATGA	GTCCACTTTA	AATCCTTAA	CGAGGATCCA	TTGGAGGGCA	4260
AGTCTGGTGC	CAGCAGCCGC	GGTAATTCCA	GCTCCAATAG	CGTATATTAA	AGTTGCTGCA	4320
GTAAAAAGC	TCGTAGTTGG	ATCTTGGGAG	CGGGCGGGCG	GTCCGCGCG	AGGCGAGCCA	4380
CCGCCCGTCC	CCGCCCCCTT	CCTCTCGCG	CCCCCTCGAT	GCTCTTAGCT	GAGTGTCCC	4440
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CTGAGGGCAT	GATTAAGAGG	GACGGCCGGG	GGCATTCTGTA	TTGCGCCGCT	AGAGGTGAAA	4620
TTCTTGGACC	GGCGCAAGAC	GGACCAAGAGC	GAAAGCATTT	GCCAAGAAATG	TTTTTATTAA	4680
TCAAGAACGA	AAGTCGGAGG	TTCGAAGACG	ATCAGATACC	GTCGTAGTTC	CGACCATAAA	4740
CGATGCCGAC	CGGCGATCGC	GGGGCGTTAT	TCCCAGACC	CGCCGGGCCAG	CTTCCGGAA	4800
ACCAAAGTCT	TTGGGTTCCG	GGGGGAGTAT	GGTTGCAAAG	CTGAAACTTA	AAGGAATTGA	4860
CGGAAGGGCA	CCACCAGGAG	TGGAGCCTGC	GGCTTAATT	GACTCAACAC	GGGAAACCTC	4920
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GTGGTGCATG	GCCGTTCTTA	GTGTTGGAG	CGATTGTCT	GTTAAATTCC	GATAACGAAC	5040
GAGACTCTGG	CATGCTAATC	AGTTACCGA	CCCCCGAGCG	GTCGGCGTCC	CCCAACTTCT	5100
TAGAGGGACA	AGTGGCGTTC	AGCCACCCGA	GATTGAGCAA	TAACAGGTCT	GTGATGCCCT	5160
TAGATGTCCG	GGGCTGCACT	CGCGCTACAC	TGACTGGCTC	AGCGTGTGCC	TACCCCTACGC	5220
CGGCAGGCGC	GGGTAACCCCG	TTGAACCCCA	TTCGTGATGG	GGATCGGGGA	TTGCAATTAT	5280
TCCCCATGAA	CGAGGGAAATT	CCCGAGTAAG	TGCGGGTCAT	AAGCTTGCCT	TGATTAAGTC	5340
CCTGCCCTT	GTACACACCG	CCCGTCGCTA	CTACCGATTG	GATGGTTAG	TGAGGCCCTC	5400
GGATCGGCC	CGCCGGGGTC	GGCCCACGGC	CCTGGCGGAG	CGCTGAGAAG	ACGGTCGAAC	5460
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CCCGCGCCGC	GGGCACGGCC	CCGCTCGCTC	TCCCCGGCCT	TCCCGCTAGG	GCGTCTCGAG	6060
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TGAAACACGG	ACCAAGGAGT	CTAACACGTG	CGCGAGTCGG	GGGCTCGCAC	GAAAGCCGCC	9300
GTGGCGCAAT	GAAGGTGAAG	GCCGGCGCGC	TCGCGGGCCG	AGGTGGGATC	CCGAGGCCTC	9360
TCCAGTCCGC	CGAGGGCGCA	CCACCGGCC	GTCTCGCCCG	CGCGCGCCGG	GAGGTGGAGC	9420
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TCCCTCCCGC	CACGCCCCGC	TCCCCGCC	CGGAGCCCCG	CGGACGCTAC	GCCGCGACGA	10200
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TAACGCGACC	GATCCCGGAG	AAGCCGGCG	GAGCCCCGGG	GAGAGTTCTC	TTTCTTTGT	10560
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GTCGCGGTT	CGGCGGGCG	CGGTGAGCT	TCGCTGGCCC	TTGAAAATCC	GGGGGAGAGG	10680
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TCGTCCCCCC	GCCCTACCCC	CCCGGCCCG	TCCGCCCGCC	GTTCCCCCCT	CCTCCTCGGC	11400
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CCTCGGGGCC	GCCGGTGAAA	TACCACTACT	CTGATCGTT	TTTCACTGAC	CGGGTGAGGC	12000
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ATACAATACA	ATACAATACG	CCGGGCGCG	TGGCTCATG	CTGTCATCCC	GTCAC	38400
GATGCCGAGG	TGGACGCATC	ACCTGAAGTC	GGGAGTTGGA	GACAAGCCCG	ACCAACATGG	38460
AGAAATCCCG	TCTCAATTGA	AAATACAAAA	CTAGCCGGGC	GGGGTGGCAC	ATGCCTATAA	38520

TCCCAGCTGC	TAGGAAGGCT	GAGGCAGGAG	AATCGCTTGA	ACCTGGGAAG	CGGAGGTTGC	38580
AGTGAGCCGA	GATTGCGCCA	TCGCACTCCA	GTCTGAGCAA	CAAGAGCGAA	ACTCCGTCTC	38640
AAAAATAAAT	ACATAAATAA	ATACATACAT	ACATACATAC	ATACATACAT	ACATACATAC	38700
ATAAAATTAA	ATAAATAAAT	AAAATAAAAT	AAATAATGG	GCCCTGCGCG	GTGGCTCAAG	38760
CCTGTCATCC	CCTCACTTTG	GGAGGCCAAG	GCCGGTGGAT	CAAGAGGCCG	TCAGACCAAC	38820
AGGGCCAGTA	TGGTGAAACC	CCGTCTCTAC	TCACAATACA	CAACATTAGC	CGGGCGCTGT	38880
GCTGTGCTGT	ACTGTGCTGTA	ATCCCAGCTA	CTCGGGAGGC	CGAGCTGAGG	CAGGAGAAC	38940
GCTGGAACCT	GGGAGGCCGA	GGTTGCGAGTG	AGCCGAGATC	GCGCCACTGC	AACCAGCCT	39000
GGGCACAGA	GCGAGACTCC	GTCTCCAAA	AATGAAAATG	AAAATGAAAC	GCAACAAAAT	39060
ATTAAAAAAG	TGAGTTTCTG	GGGAAAAAAGA	AGAAAAAGAA	AAAGAAAAAA	ACAACAAAAC	39120
AGAACAAACCC	CACCGTGACA	TACACGTACG	CTTCTCGCCT	TCGAGGCT	CAAACACGTT	39180
AGGAATTATG	CGTGATTCT	TTTTTTAACT	TCATTTATG	TTATTATCAT	GATTGATGTT	39240
TCGAGACGGA	GTCTCGGAGG	CCCGCCCTCC	CTGGTTGCC	AGACAACCCC	GGGAGACAGA	39300
CCCTGGCTGG	GCCCCGATTGT	TCTTCTCCTT	GGTCAGGGGT	TTCCTTGCT	TTCTCGTGT	39360
CTTTAACCCG	CGTGGACTCT	TCCGCCTCGG	GTTTGACAGA	TGGCAGCTCC	ACTTTAGGCC	39420
TTGTTGTGTTG	TGGGGACTTT	CCTGATTCTC	CCCAGATGTA	GTGAAAGCAG	GTAGATTGCC	39480
TTGCCTGGCC	TTGCCTGGCC	TTGCCTTTTC	TTTCTTCTT	TCTTTCTT	TTACTTTCTC	39540
TTTTCTCT	TCTTCTCTT	CTTTTTTTTG	AGACAGAGTT	TCACCTTGTT	TGCCAGGCT	39600
AGAGGGCAAT	GGCGCGATCT	CGGCTCACCG	CACCCCTCCGC	CTCCCGAGGT	CAAGCGATT	39660
TCCTGCCTCA	GCCTCCTGAT	TAGCTGGAT	TACAGGCATG	GGGCCACCGTG	CTGGCTGATG	39720
TTTGTACTTT	TAGTAGAGAC	GGTGTGTTTC	CATGTGGTC	AGGCTGGTCT	CCCACTCCCA	39780
ACCTCAGGTG	GTCCGCCTGC	CTTAGCCTCC	CAAAGTGCTG	GGATGACAGG	CGTGAACCG	39840
CGCCCAGCCT	CTCTCTCTCT	CTCTCTCTCT	CTCGCTCGCT	TGCTTGCTT	CTTTCGTGCT	39900
TTCTTGCTT	CCCCTTTCTT	TGCTTTCTT	CTTCTTTCG	TTTCTTCAT	GCTTGCTTTC	39960
TTGCTTGCTT	GCTTGCTTTC	GTGCTTTCTT	GCTTTCTCT	TTTCTTTCTT	TCTTTCTTTC	40020
TTTCTTCTT	TTGTTTCTT	CTTGCTTGCT	TTCTTGCTT	CTTGCTTGCT	TTCGTGCTT	40080
CTTGCTTCC	TGTTTCTT	CTTCTTCTT	TTCTTTCTT	TCTTTCTT	TTGCTTCCCT	40140
GCTTGCTTGC	TTTGTGCTT	TCCTGTTTTC	TCGATTTCTT	TCTTTCTT	TTTCTTCC	40200
TGCTTGCTT	CTTGCTGCT	TCCTGTTCTG	CTTCTGCTT	TCCTGTTT	TTTCTTCTT	40260
TCTTCTTTT	GTTTCTTCT	TGCTTGCTT	CTTGCTGCT	TGCTTCTG	CTGCTTGT	40320
TCTCGATTTC	TTTCTTCTT	TTGTTTCTT	CCTGCTGCT	TTCTTGCTT	ATTGCTTCTG	40380
TGCTTCTT	CTTTCTGTT	TTCTTTCTT	CTTTGTTT	TTTCTTCTT	GCTTCTTGT	40440
TTTCTTGCTT	TCTTGCTTGC	TTGCTTTCGT	GCTTTCTTGT	TTTCTTGCTT	TCTTCTTT	40500
GTTTCTTCT	TGCTTGCTT	CTTGCTTCC	TGTTTCTT	CTTCTTGCT	TGCTTGCTT	40560
CGTGCTTCT	TTCTTGCTT	CTTTCTTTC	TTTCTTTCT	TTTCTTTCT	TTCTTGCTT	40620
CTTTCTTC	ATCATCATCT	TTCTTCTT	CCTTTCTT	TTTCTTCTT	TCTATCTT	40680
TTTCTTCTT	TCTTCTT	TTCTTCTT	TCTTCTT	TCGTCCTT	GAGACAGAGT	40740
TTCACTCTG	TTTCCACGGC	TAGAGTGCA	TGGCGCGATC	TTGGCTCAC	GCACCTTCCG	40800
CCTCCCGGGT	TCGAGCGCTT	CTCCTGCCTC	CAGCCCTCCCG	ATTAGCGGGG	ATTGACAGGG	40860
AGGCACCCCC	ACGCCTGGCT	TGGCTGATGT	TTGTGTTTT	AGTAGGCACG	CCGTGTCTCT	40920
CCATGTTGCT	CAGGCTGGTC	TCCAACCTCCC	GACCTCTGT	GATGCGCCCA	CCTCGGCCTC	40980
TCGAAGTGCT	GGGATGACGG	GGGTGACGAC	CGTGCCCGGC	CTGTTGACTC	ATTCGCTT	41040
TTTATTTCTT	TCGTTTCCAC	GGCTTTACTT	ATATGATTA	ATGTAACAGT	TTCTGTACGC	41100
TTATATGCAA	ACAACGACAA	CGTGTATCTC	TGCATTGAA	ACTCTTGCGT	ATGGTAAATA	41160
CGTATCGGT	GTATGGAAAT	AGACTCTGT	ATGATAGAT	TAGGTGTC	TGTTATACAA	41220
ATAAAATACAC	ATCGCTTAT	AAAAGAAGGG	TCGTCATAA	AGACGTTTAT	TTTACGTATG	41280
AAAAGCGTCG	TATTATGTTG	TGTAATGAA	CCGAGCGTAC	GTAGTTATC	CTGTTTCTT	41340
TCTCCTCTC	CTTCGTGTT	TTCTTCTT	CTTCTCTCCT	TTCTCTCCT	CTTCTAGGTT	41400
TTCTTCTCT	CTTCCTTCC	TTCTTCTCT	CTTCTGT	TTTTTCTT	CGTCTTTAT	41460
TTCTTCTT	TTCCCTGT	TTCTTCTT	TTTCTTCT	CTCTGTTCT	TTTCTCCCTC	41520
TTTCTTCTG	TTTCTTCTC	ATTCTTCTC	TCTTTCTG	TGTTTCTT	CTTCCCGTCT	41580
GTCTTTAAA	AAATTGGAGT	GTTCAGAG	TTTACTTGT	GTATCTACGT	TTTCTAAATT	41640
GTCTCTCTT	TCTCCATT	CTCCTCCCT	CCCTCCCTCC	CTCCCTG	CCTTCCCTCC	41700
CTCCCTCCCT	TTGCCCATCT	GTCTCTT	CCCACCTCCC	TCCCCCGTC	TGTCTCTGCG	41760
TGGATTCCGG	AAGGCCCTAC	CGATTCTGC	TCTCCCGT	TCTCGAGCGA	CCCCGGCGACC	41820
GAGCTCTTGT	GTGTTCTT	TCCCTCCCTC	CCTCCCTCCC	TCCCTCCCTC	CCTCCCTGCT	41880
TCCGAGAGGC	ATCTCCAGAG	ACCGCGCCGT	GGGTTGTC	CTGACTCTG	CGCGGTCGAG	41940
GCAGAGACGC	GTTTTGGGCA	CCGTTTGT	GGGGTTGGGG	CAGAGGGGCT	GCGTTTCGG	42000
CCTCGGGAAAG	AGCTTCTCGA	CTCACGGTT	CGCTTCTGCG	GTCCACGGGC	CGCCCTGCCA	42060
GCCGGATCTG	TCTCGCTGAC	GTCCCGGGCG	GTTGTCGGGC	TCCATCTGGC	GGCCGCTT	42120
AGATCGTGCT	CTCGGCTTCC	GGAGCTGCG	TGGCAGCTG	CGAGGGAGGG	GACCGTCCCC	42180
GCTGTGAGCT	AGGCAGAGCT	CCGGAAAGCC	CGCGGTGCG	AGCCCGGCTG	GCCCGGTGCG	42240
GCCAGAGCTG	TGGCCGTC	CTTGTGAGTC	ACAGCTCTG	CGTGCAGGTT	TATGTGGGG	42300
AGAGGCTGTC	GCTGCCGCTTC	TGGGCCGCG	GCGGGCGTGG	GGCTGCCGCG	GCCGGTCGAC	42360
CAGCGCGCCG	TAGCTCCCAGA	GGCCCGAGCC	GCGACCCGGC	GGACCCGGCC	CGCGTGGCG	42420

AGGCTGGGGA	CGCCCTTCCC	GGCCCGGTGCG	CGGTCCGCTC	ATCCTGGCCG	TCTGAGGC GG	42480
CGGCCGAATT	CGTTTCCGAG	ATCCCCGTGG	GGAGCCGGGG	ACCGTCCCGC	CCCCGTCCCC	42540
CGGGTGC CGG	GGAGCGGTCC	CCGGGCCGGG	CCGCGGTCCC	TCTGCCGCGA	TCCTTTCTGG	42600
CGAGTCCCCG	TGGCCAGTCG	GAGAGCGCTC	CCTGAGCCGG	TGCGGCCCGA	GAGGTGCGC	42660
TGGCCGGCCT	TCGGTCCCTC	GTGTGTCCCC	GTCGTAGGAG	GGGCCGGCG	AAAATGCTTC	42720
CGGCTCCCGC	TCTGGAGACA	CGGGCCGGCC	CCTGC GTGTG	GCCAGGGCGG	CCGGGAGGGC	42780
TCCCCGGCCC	GGCGCTGTCC	CCCGGTGTGT	CCTTGGGTTG	ACCAGAGGGA	CCCCGGGCGC	42840
TCCGTGTGTG	GCTGCGATGG	TGGCGTTTT	GGGGACAGGT	GTCCGTGTCC	GTGTCGCGC	42900
TCGCCTGGGC	CGCGGGCGTG	GTCGGTGACG	CGACCTCCCG	GCCCCGGGGG	AGGTATATCT	42960
TTCGCTCCGA	GTCGGCAATT	TTGGGCGGCC	GGGTTATAT			42999

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTCCCGCGCG	GCCCCCGTGT	TCGCCGTTCC	CGTGGCGCGG	ACAATGCGGT	TGTGCGTCCA	60
CGTGTGCGTG	TCCGTGCAGT	GCCGTTGTGG	AGTGCTCGC	TCTCCTCCTC	CTCCCCGGCA	120
CGCTTCCCAC	GGTTGGGGAC	CACCGGTGAC	CTCGCCCTCT	TCGGGCCTGG	ATCCG	175

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTCTGGTGG	GAATTGTTGA	CCTCGCTCTC	GGGTGCGGCC	TTTGGGGAAC	GGCGGGGTG	60
GTCGTGCCCG	GCGCCGGACG	TGTGTGCGGGG	CCCACTTCCC	GCTCGAGGGT	GGCGGTGGCG	120
CGGGCGTTGG	TAGTCTCCCG	TGTTGCGTCT	TCCCAGGCTC	TTGGGGGGGG	TGCCGTCGTT	180
TTCGGGGCCG	GCGTTGCTTG	GCTTACGCA	GCTTGGTTTG	GGACTGCCTC	AGGAGTCGTG	240
GGCGGTGTGA	TTCCCGCCGG	TTTGCGCTCG	CGTCTGCCTG	CTTTGCCTCG	GGTTTGCTTG	300
GTTCTGTCT	CGGGAGCGGT	GGTTTTTTTT	TTTTTGC GGT	CCCGGGGGAGA	GGGGTTTTTC	360
CGGGGGACGT	TCCCCGTGCGC	'CCCTGCGGCC	GGTGGGTTTT	CGTTTCGGGC	TGTGTTTCGTT	420
TCCCCCTTCCC	CGTTTCGGCG	TCGGTTCTCC	CCGGTCGGTC	GGCCCTCTCC	CCGGTCGGTC	480
GCCCCGGCGT	GCTGCCGGAC	CCCCCCTTC	GGGGGGGGATG	CCCGGGGCACG	CACCGCGTCCG	540
GGCGGCCACT	GTGGTCCGGG	AGCTGCTCGG	CAGGGGGGTG	AGCCAGTTGG	AGGGGGCGTCA	600
TGCCCTCCGCG	GGCTCCCGTG	GCCGACGCCG	CGTGTCTTT	GGGGGGGGCC	GTGCGTGC	660
GAAGGCTGCG	CACGTTGTCG	GTCCTTGCGA	GGGAAAGAGG	CTTTTTTTTT	TTAGGGGGTC	720
GTCCTTCGTC	GTCCCGTCGG	CGGTGGATCC	GGCCT			755

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCGGAGGTG	CGTCTGCGGG	TTGGGGCTCG	TCCGGCCCCG	TCGTCCCTCCG	GGAAGGCGTT	60
TAGCGGGTAC	CGTCGCCGCG	CCGAGGTGGG	CGCACGTCGG	TGAGATAACC	CCGAGCGTGT	120
TTCTGGTTGT	TGGCGCGGGG	GGCTCCGGTC	GATGTCCTCC	CCTCCCCCTC	TCCCCGAGGC	180
CAGGTCAAGCC	TCCGCCGTGT	GGCTCTCGTC	GCCGTCCTCCC	CCCCCTCAC	GTCCCTCGCG	240
AGCGAGGCCG	TCCGTTCGAC	CTTCCTCCG	CCTTCCCCCC	ATCTTTCCG	GCTCCGTTGG	300
CCCCGGGGTT	TTCACCGGCC	CCCCCACGCT	CCTCCGCCTC	TCCGCCCCGTG	GTTTGGACGC	360
CTGGTTCGG	TCTCCCCGCC	AAACCCCGGT	TGGGTGGTC	TCCGGCCCCG	GCTTGCTCTT	420
CGGGTCTCCC	AACCCCCGGC	CGGAAGGGTT	CGGGGTTCC	GGG		463

- (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGATTCTTCA	GGATTGAAAC	CCAAACCGGT	TCAGTTTCC	TTCCGGCTCC	GGCGGGGGGG	60
GGCGGCCCG	GGCGTTTGG	TGAGTTAGAT	AACCTGGGC	CGATCGCACG	CCCCCGTGG	120
CGGCGACGAC	CCATTCAAC	GTCTGCCCTA	TCAACTTCG	ATGGTACTCG	ATGTGCCTAC	180
CATGGTGACC	ACGGGTGACG	GGGAATCAGG	GTTCGATTCC	GGAGAGGGAG	CCTGAGAAC	240
GGCTTACACCA	TCCAAGGAAG	GCAGCAGGCG	CGCAAATTAC	CCACTCCCGA	CCCGGGGAGG	300
TAGTGACGAA	AAATAACAAT	ACAGGACTCT	TTCGAGGCC	TGTAATTGGA	ATGAGTCCAC	360
TTTAAATCCT	TTAACGAG					378

- (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATCCATTGG	AGGGCAAGTC	TGGTGCCAGC	AGCCGCGGT	ATTCCAGCTC	CAATAGCGTA	60
TATTAAGTT	GCTGCAGTTA	AAAAGCTCGT	AGTTGGATCT	TGGGAGCGGG	CGGGCGGTCC	120
GCCGCGAGGC	GAGTCACCGC	CCGTCCCCGC	CCCTTGCCCTC	TCGGCGCCCC	CTCGATGCTC	180

TTAGCTGAGT	TGTCCCGCGG	GGCCCGAAGC	GTTTACTTTG	AAAAAATTAG	AGTTGTTCA	240
AAGCAGGCC	GAGCCGCCTG	GATACCGCCA	GCTAGGAAAT	AATGGAATAG	GACCGCGGTT	300
CCTATTTGT	TTGGTTTTCG	GAACTGAGCC	CATGATTAAG	GGAAACGGCC	GGGGGCATTC	360
CCTTATTGCG	CCCCCTTA					378

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGATCTTCC	CGCTCCCCGT	TCCTCCCGGC	CCCTCCACCC	GCGCGTCTCC	CCCCCTTCTTT	60
TCCCCTCTCC	GGAGGGGGGG	GAGGTGGGGG	CGCGTGGGCG	GGGTGCGGGG	TGGGGTCCGGC	120
GGGGGACCGC	CCCCGGCCGG	CAAAGGCGG	CCGCCGGGCG	CACTTCAACC	GTAGCGGTGC	180
GCCCGGACCG	GCTACCGAGAC	GGCTGGGAAG	GCCCCGACGGG	GAATGTGGCT	CGGGGGGGGC	240
GGCGCGTCTC	AGGGCGCGCC	GAACCACCTC	ACCCCGAGTG	TTACAGCCCT	CCGGCCGCGC	300
TTTCGCGGAA	TCCCAGGGCC	GAGGGGAAGC	CCGATACCCG	TGCGCCGCGT	TTTCCCCCTCC	360
CCCCGTCCCG	CTCCCCGGCC	GGCGTGGGGG	TGGGGGCCGG	CCCGCCCCCTC	CCACGCCCCGT	420
GGTTTCTCTC	TCTCCCGGTC	TCGGCCGGTT	TGGGGGGGGG	AGCCCGGGTTG	GGGGCGGGGC	480
GGACTGTCTC	CAGTGCGCC	CGGGCGTCGT	CGGCCCGTCG	GGCCCCGGGGG	GTTCTCTCGG	540
TCACGCCGCC	CCCGACGAAG	CCGAGCGCAC	GGGGTCGGCG	GCGATGTCTGG	CTACCCACCC	600
GACCCGTCTT	GAAACACCGA	CCAAGGAGTC	TAACCGGTGC	GCGAGTCAGG	GGCTCGCACG	660
AAAGCCGCCG	TGGCGCAATG	AAGGTGAAGG	GGCCCGTCCG	GGGGCCCCGAG	GTGGGATCC	719

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGAGGCCTCT	CCAGTCGCC	GAGGGCGCAC	CACCGCCCCG	TCTCGCCCGC	CGCGTCGGGG	60
AGGTGGAGCA	CGAGCGTACG	CGTTAGGACC	CGAAAGATGG	TGAACATATGC	CTGGGCAGGG	120
CGAAGCCAGA	GGAAACTCTG	GTGGAGGTCC	GTAGCGGTCC	TGACGTGCAA	ATCGGTCTGC	180
CGACCTGGGT	ATAGGGCGA	AAGACTAATC	GAACCATCTA	GTAGCTGGTT	CCCTCCGAAG	240
TTTCCTCTAG	GATAGCTGGC	CGCTCTCGCAA	CCTTCGGAAG	CAGTTTTATC	CGGGTAAAGG	300
CGGAATGGAT	TAGGAGGTCT	TGGGGCGGGA	AACGATCTCA	AACTATTTCT	CAAACCTTAA	360
ATGGGTAAGG	AAGCCCGGCT	CGCTGGCGTG	GAGCCGGGGG	TGGAATGCGA	GTGCCTAGTG	420
GGCCACTTTT	GGTAAGCAGA	ACTGGCGCTG	CGGGATGAAC	CGAACGCCGG	GTAAAGGCGC	480
CCGATGCCGA	CGCTCATCAG	ACCCAGAAA	AGGTGTTGGT	TGATATAGAC	AGCAGGACGG	540
TGCCCATGGA	AGTCGGAATC	CGCTAAGGAG	TGTGTAACAA	CTCACCTGCC	GAATCAACTA	600
GCCCTGAAAA	TGGATGGCGC	TGGAGCGTCG	GGCCCATACC	CGGCCGTGCG	CGGCAGTCGG	660
AACGGGACGG	GACGGGAGCG	GCCG				685

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGGAATTCC CCTATCCCTA ATCCAGATTG GTG

33

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAACTGCAGG CCGAGCCACC TCTCTCTGT GTTG

35

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGGAATTCAC AGAAGAGAGG TGGCTCGGCC TGC

33

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCCTGCAGG AAGTCATACC TGGGGAGGTG GCCC

34

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAACTGCAGG TTAATTAAACC CTAACCCTAA CCCTAACCT AACCTAACCC CTAACCCTAA

60

CCCTAACCC AACCCGGGAT

80

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTGGGCCCTA GGCTTAAGG

19

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCCAGGGTTT TCCCAGTCAC GACGT

25

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(iii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTGCAAGGC GATTAAGTTG GGTAAC

26

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TATGTTGTGT GGAATTGTGA GCGGAT

26

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGGTTTAAAC AGATCTCTGC A

21